IN THE CLAIMS:

Please cancel claim 22 without prejudice or disclaimer, and amend claims 16 and 24 as follows:

1-9. (Canceled)

10. (Previously Presented) The method of claim 16 or claim 24, wherein the amount of the probes is detected prior to the contacting step.

11. (Previously Presented) The method of claim 16 or claim 24, wherein the amount of the biopolymers or the sample nucleic acids hybridized to the probes is detected after the completion of the contacting step.

12. (Previously Presented) The method of claim 16 or claim 24, wherein both the amount of the probes and the amount of the sample or the sample nucleic acids hybridized to the probes are detected after the completion of the contacting step.

13. (Previously Presented) The method of claim 16 or claim 24, wherein the sample nucleic acids and the probes are labeled with different labeling materials.

14. (Original) The method of claim 16 or claim 24, wherein the value is indicated on a display.

15. (Previously Presented) The method of claim 16 or claim 24, wherein the substrate comprises a biochip.

16. (Currently Amended) A method for detecting a degree of hybridization between a plurality of types of probes and a sample comprising [[a]] <u>one</u> type of biopolymers, the method comprising

(a) providing a substrate on which each type of the probes is separately immobilized on each different and separate predetermined position, wherein each of the probes is labeled with a first detectable label;

(b) providing the sample comprising the biopolymers, wherein each of the biopolymers is labeled with a second detectable label;

(c) contacting the sample with the probes;

(d) detecting an amount of the probes at each different and separate predetermined position of the substrate by detecting the first detectable label;

(e) detecting an amount of the biopolymers hybridized to the probes at each different and separate predetermined position of the substrate by detecting the second detectable label; and

(f) producing a value representing the degree of hybridization between the probes at each different and separate predetermined position and the biopolymers by dividing the difference between the amount of the probes detected at each different and separate predetermined position and the amount of the biopolymers hybridized to the probes by the amount of the probes.

17. (Original) The method of claim 16, wherein the detectable label comprises a fluorescent material.

18. (Previously Presented) The method of claim 17, wherein an emission wavelength of the fluorescent material labeling the biopolymers is detected separately from an emission wavelength of the fluorescent material labelling the probes.

19. (Previously Presented) The method of claim 16, wherein each of the biopolymers comprises a nucleic acid.

20. (Original) The method of claim 19, wherein the nucleic acid comprises a DNA or an RNA.

21. (Canceled)

22. (Cancelled)

23. (Cancelled)

24. (Currently Amended) A method for detecting a degree of hybridization between a plurality of types oligonucleotide probes immobilized onto an array and [[a]] one type of sample nucleic acids, the method comprising:

(a) providing a substrate on which each type of the oligonucleotide probes is separately immobilized on each different and separate predetermined position to form an array, wherein each of the oligonucleotide probes is labeled with a first detectable label;

(b) providing the sample nucleic acids, wherein each of the nucleic acids is labeled with a second detectable label;

(c) contacting the sample nucleic acids with the probes;

(d) detecting an amount of the probes at each different and separate predetermined position of the substrate by detecting the first detectable label;

(e) detecting an amount of the sample nucleic acids hybridized to the probes at each different and separate predetermined position of the substrate by detecting the second detectable label; and

(f) producing a value representing the degree of hybridization between the probes at each different and separate predetermined position and the sample nucleic acids by dividing ~~normalizing~~ the difference between the amount of the probes detected at each different and separate predetermined position and the amount of the sample nucleic acids hybridized to the probes by with the amount of the probes.